

STEVEN M. FOLTZ

Washington University in St. Louis
Ph.D. candidate studying cancer genomics

Email: stevenmasonfoltz@gmail.com
Cell phone: (206) 953-6490

SUMMARY

I am a bioinformatics researcher with expertise analyzing large-scale cancer genomics sequencing data. I am driven by a passion for delivering robust and reproducible research for the benefit of society. My values include: teamwork, inclusion, open science, and leading by example.

RESEARCH EXPERIENCE

Washington University in St. Louis, St. Louis, MO

June 2014 – present

Graduate student, Laboratory of Li Ding, PhD

- Pan-cancer computational projects utilizing tumor and normal tissue sequencing data (DNA, RNA) to understand multiple types of germline and somatic variation
- Large-scale, integrative data analysis tool and pipeline development, including variant calling and quality control using bulk DNA and RNA, single cell RNA, and linked-read DNA sequencing

Results: 2 published first author papers in *Bioinformatics* and *Cell Reports* and 4 co-author papers in *Cell*, *Nature Medicine*, *Molecular Psychiatry*, and *Annals of Oncology*.

Virginia Commonwealth University, Richmond, VA

August 2013 – May 2014

Biostatistician, Laboratory of Nengliang Yao, PhD

University of Washington, Seattle, WA

September 2011 – August 2013

Research assistant, Laboratory of Brian Browning, PhD, and Sharon Browning, PhD

RESEARCH SKILLS

- Programming languages: R, Python, Bash, Unix command line (github.com/envest)
 - Analysis of large-scale sequencing data (DNA, RNA) and file formats (VCF, BAM, MAF, BED) on large Unix clusters, and data visualization
 - Computational project management, data analysis team leadership, and multi-institutional collaboration
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EDUCATION

PhD, Washington University in St. Louis, St. Louis, MO

June 2014 – present

Division of Biology and Biomedical Science (Human and Statistical Genetics)

MS Biostatistics, University of Washington, Seattle, WA

September 2011 – August 2013

BS Mathematics, Presbyterian College, Clinton, SC

August 2006 – April 2010